

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 9, 2002, 17:57:04 ; Search time 1595 Seconds
(without alignments)
6811.943 Million cell updates/sec

Title: US-09-635-501-2
Perfect score: 4291
Sequence: 1 MSSSSWLLLSLVAVTAQST.....LSKGNPNPQNTDDVQTSF 805

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09635501/runat_09102002_094529_18537/app_query.fasta_1.967
-DB=EST -QPMT=fastcap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.edi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09635501 -CGN_1_11106.ernat_09102002_094529_18537 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAB -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpi:*
7: em_estro:*
8: em_esthc:*
9: gb_est1:*
10: gb_est2:*
11: gb_estc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	1452	33.8	987 9	AL551235
2	1071	25.0	1603 11	AK008530 Mus muscu

ALIGNMENTS

RESULT 1
AL551235
LOCUS AL551235 LTI_NFL006_PL2 Homo sapiens cDNA clone CSOD1041YM14 5
DEFINITION prime, mRNA sequence.
ACCESSION AL551235
VERSION AL551235.1 GI:12888986
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 987)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
FEATURES
1. 987
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSOD1041YM14"
/clone_lib="LTI_NFL006_PL2"

(Invitrogen). Research Genetics tracking code 017. Note:

VERSION BG401683.1 GI:13295131

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BASE COUNT
ORIGIN
237 a 167 c 170 g 189 t
this is a NIH_MGC Library."

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KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Alignment Scores:		
Pred. No.:	Length:	763
Score:	Matches:	225
	1034.50	
Percent Similarity:	Conservative:	6
Best Local Similarity:	Mismatches:	12
Query Match:	Indels:	10
DB:	Gaps:	3
	10	

REFERENCE
1 (bases 1 to 879)
AUTHORS
TITLE
JOURNAL
COMMENT

US-09-635-501-2 (1-805) x BI913504 (1-763)

CDNA Library Preparation

QY	1	MetSerSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr	20
DB	19	ATGTCAAGCTCTTCCTGGCTCTTCTCAGCCCTTGTGTGAATGCTGCTCAGTCCACC	78
QY	21	Ile-GluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe	40
		:::	
DB	79	ATGTGTGGAGACAGCCCAAGACATTTTTGGACAAGTTTAAACCACGAAGCCGAAGACCTGTT	138

FEATURES

Qy	40	eTyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValG1	50
Db	139	CTATCAAGGTTCACCTGCTCTCGAATTATTAACACCAATAATTACTGAAGAGAATGTCCA	198
Qy	60	nAsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAl	80
Db	199	AAACATGAATTAATGCTGGGACAATGTGTGCTCTTTTAAAGGAACAGTCCACACTGC	258

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source
i. 0075
/organism="Homo
/db_xref="taxo
/clone_image=:
/clone_lib="NI
/lab_host="DHL
/note="Organ:
Sfil (access
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Qy	80	aGlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuAlaLe	100
Db	259	CCAAATGTATCCACTACAGAAGAAATTCAGAAATTCACAGTCAAGCTTCACGTGCAAGGCTCT	318
Qy	100	uGlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLe	120
Db	319	TCAGCAAAATGGTGCTTCAGTGCCTCAGAGACACAGACGAAACGGTTGTAACACCAATTCT	378

sequence: 5'-
5'-ATTCTAGAGC
C, or G and N
kb (range 0.5-
by PCR. This l
and was constr
CA). Note: thi

Qy	120	uasnThwetserThrileTyrSerThrGlyLysValCysasnProaspAsnProGIngl	140
Db	379	AAATACAATGAGCACCATCTACACTAGTGGAAAAAGTTGTAAACGACGATAATCCACAAGA	438
Qy	140	uCysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGl	160
Db	439	ATGCTTATATCTTGAACACAGCTTTGTAATGACATATATGSCAACAGTTTGTAGACTACAATGA	498

BASE COUNT	Z/3 a	1/7 °
ORIGIN		
Alignment Scores:		
Pred. No.:	9.29e-110	
Score:	1048.50	
Percent Similarity:	80.50%	
Best local Similarity:	77.30%	

Qy	160	uArGLeuTrpAlaTrp--GluSerTrpArgSerGluValGlyLysGlnLeuArgProLe	179
Db	499	GAGGCTCTGGGCTTGGGCAACGCTGCAGACTCTGAGGTGCGCAAGCAGCTGAGG	558
Qy	179	uTyrGluGluTyrValValLeu-LysAsnGluMetAlaArgAlaAsnHisTyrGluAspT	199
Db	559	ATATGACACATCTGCTCTTGAAGAGATGAGATGCGCAAGCGCAATCTATTCGGG	618

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Query match:      24.43%
DB:               10
US-09-635-501-2 (1-805) x BG401683
Qy    388 GlnProPheLeuLeuArgAsnGlyVal
      |||||
Db    3 CaaCettTTCCTCAAGAAATCGACG
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[illegible]

Qy	408	MetSerLeuSerAlaAlaThrProL
Db	62	ATGTCACCTTCTGAGCCACACCTA
Qy	428	pheGlnGluAspAsnGluThrGluI
Db	122	TTTTTCTGCTGCTGCTGCTGCTG

QY 236 LeuTyr-GluHisLeuHisAlaTyr 243
||||| ||| |||||
Db 739 TTATACTGAACCTCTTCATGCCTAT 753

RESULT 4
BG401583

Qy 448 GlyThrLeuProPheThrTyrMetL
Db 181 GGGACTCTGCCATTACTTACATGT
Qy 468 IleProLysAspGlnTrpMetLysL

DEFINITION 602466350F1 NIH_MGC_75 Homo sapiens CDNA clone IMAGE:4594140 5', mRNA sequence.
ACCESSION BG401683

Qy 488 valGluProValProHisAspGluT

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Db 282 ----- 282
QY 508 AsnAspTyrSerPheLeuArgTyrThrArgThrLeuTyrGlnPheGlnGlu 527
Db 283 -----ACCCCTTACCAGTTCACAGAA 309
QY 528 AlaLeuCysGlnAlaLeuAlaLeuHisGlyProLeuHisLysCysAspIleSerAsnSer 547
Db 310 GCACCTTGTCAACAGCAATGAAGGCCCTCTGCACAAATGTGACATCTCAAACTCT 369
QY 548 ThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeuGlyLysSerGluProTyrThr 567
Db 370 ACAGAGCTGCACAGAACTGTTCAATATGCTGAGGCTTGGAATAACAGAACCTGGACC 429
QY 568 LeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsnValArgProLeuLeuAsnTyr 587
Db 430 CTAGCATTTGGAATGTTGTAGAGCAAGACATGAATGAAGGCCACTGCTCAACTAC 489
QY 588 PheGluProLeuPheThrTrpLeuLysAspGlnAsnLysAsnSerPheValGlyTrpSer 607
Db 490 TTTGAGCCCTTTTACCTGGCTGGAAGACCAAGAAATCTTTTGTGGGATGAGT 549
QY 608 ThrAspTrpSerProTyrAlaAsp-GlnSerIleLysValArgIleSerLeuLysSerAl 627
Db 550 ACCGACTGGAGTCCATATGACAGAACCAAGCATCAAGTGAGGATAGCCCTAAATCAGTC 609
QY 627 aLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrIlePheArgSerSerVa 647
Db 610 T--GGAGATAAGCA-TATGACTGGAGC---ACATGAATTCCTCTGTNCCGATCATCTGT 662
QY 647 lAlaTyr-AlaMetAspGlnTyrPheLeuLysValLysAsnGlnMetIleLeuPheGlyG 667
Db 663 GGCATATGCTATTACGGAGTACTTTTAAAGTAAACATCG-----ATGATCTTTGGGG 716
QY 667 lu 667
Db 717 AG 718

RESULT 5
BG962298
LOCUS
DEFINITION
602827090F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4981606 5',
mRNA sequence.
ACCESSION BG962298
VERSION BG962298.1 GI:14349935
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 766)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rgsb@rmail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10983 row: d column: 23
High quality sequence stop: 708.
Location/Qualifiers
1..766
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4981606"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
FEATURES
source

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/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 233 a 156 c 179 g 198 t
ORIGIN
Alignment Scores: 7.89e-108 Length: 766
Pred. No.: 1031.00 Matches: 210
Score: 88.85% Conservative: 21
Percent Similarity: 80.77% Mismatches: 23
Best Local Similarity: 24.03% Indels: 9
Query Match: 10 Gaps: 0
DB:
US-09-635-501-2 (1-805) x BG962298 (1-766)
QY 416 LysHisLeuLysSerIleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGlu 435
Db 2 ANGATCTGAAATCCATTCCTGCTTCGCATCCGATTTTCAAGAGATAGCGAACACAG 61
QY 436 IleAsnPheLeuLeuLysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMet 455
Db 62 ATAAACTCTCTACTGAAACAGGCATTTGCAATTTGGAACACATACCGTTTACATG 121
QY 456 LeuGluLysTrpArgTrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLys 475
Db 122 TTAGAGAAGTGGAGGTGGATGGTCTTTGGGGTGAATTTCCCAAGAGCAGTGGATGAA 181
QY 476 LysTrpTrpGluMetLysArgGluIleValGlyValValGluProValProHisAspGlu 495
Db 182 AAGTGGTGGAGATGAAGCGGAGATCGTTGGTGGTGGAGCCTCTCCCTCATGATGAA 241
QY 496 ThrTyrCysAspProAlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyr 515
Db 242 ACATACTGTGACCTGCATCTCTCTCCATGTTCTAATGATTACTCATTCATGATAT 301
QY 516 TyrThrArgThrLeuTyrGlnPheGlnPheGlnGluAlaLeuLysGlnAlaLysHis 535
Db 302 TACAAAGAGGACCAATTTACCAATTCAGTTTCAAGAAGCTTTTCAAGCAGCAGTAAGTAT 361
QY 536 GluGlyProLeuHisLysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPhe 555
Db 362 AATGGTCTCTGCACAAATGTGACATCTCAAAATTCCTGAAGCTGGGCAAGTTGCTC 421
QY 556 AsnMetLeuArgLeuGlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValG 575
Db 422 AAGATGTGAGTCTTGAAATTCAGAGCCCTTGACCAAGCCCTTGGAACATGTGGTAGG 481
QY 575 yAlaLysAsnMetAsnValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLe 595
Db 482 AGCAAGGAATATGATGATTAACCAACCACTGCTCAATTACTTCCAAACCGTTTGTGACTG 541
QY 595 uLysAspGlnAsnLysAsnSerPhe-ValGly-TrpSerThrAspTrpSerProTyrAla 614
Db 542 GAAAGACAGACAGAAATTTCTTTCAGTGGCGGTGGAAACACTGAATGGAGCCCATATGCC 601
QY 615 AspGlnSerIleLysValArgIle-SerLeuLysSerAlaLeuGlyAsp-LysAlaTyrG 634
Db 602 GACCAAGACATTAACAGTGAAGGATTAAGCCTTAAGATCAGCTCTTGAGAGCTACATGATG 661
QY 634 luTrpAsnAsp-AsnGluMetTyrLeuPheArgSerSerValAlaTyrAlaMetArgGln 653
Db 662 ACTGGACCAAGCAAGAAATTTCTTTCAGTGGCGGTGGAAACACTGAATGGAGCCCATATGCC 719
QY 654 TyrPheLeuLysValLysAsnGlnMetIleLeuPheGlyGluGluAsp 669
Db 720 GTCATGCTCAATAATCAAAACACAGACAGTCTCTTTTCTA-GAGGAGGAT 766
RESULT 6
BI561069
LOCUS
DEFINITION 60254275F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5296531 5',

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mRNA sequence.
ACCESSION BI561069
VERSION B1561069.1 GI:15448383
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NIH-MGC http://mhc.nci.nih.gov/
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1750 row: f column: 20
High quality sequence stop: 674.
FEATURES
source
Location/Qualifiers
1..676
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/db_xref="taxon:9606"
/clone="IMAGE:5296531"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcagag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',
size-selected for average insert size 2-2 kb and
normalized to 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 215 a 134 c 161 g 166 t
ORIGIN
Alignment Scores:
Pred. No.: 7.16e-107 Length: 676
Score: 1022.00 Matches: 205
Percent Similarity: 97.62% Conservative: 0
Best Local Similarity: 97.62% Mismatches: 1
Query Match: 23.82% Indels: 4
DB: 10 Gaps: 0
US-09-635-501-2 (1-805) x BI561069 (1-676)
QY 1 MetSerSerSerTrpLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
Db 55 ARGTCAGGCTTCCTCGGCTCTCTCAGCCCTGTTGCTGTAAGTCTGCTCAGTCCACC 114
QY 21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
Db 115 ATTGAGGACAGCCCAAGACATTTGGGACAGTTTAAACCCAGCCGAGACCTGTTTC 174
QY 41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
Db 175 TATCAAGTTTCACTGCTCTTGGGAATTATACACCAACCAATATTACTGAAGAGATGTCCTCA 234
QY 61 AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGlu-GlnSerThrLeuAl 80
Db 235 AACATGAATAATGCTGGGACAAATGCTGCTGCTTTTAAAGGAGACAGTCCACATTCG 294
QY 80 aGlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnAlaLe 100
Db 295 CCAAATGTATCCACTACACAGAAATTCAGAAATCTCAGAGTCAAGCTTCAGTCGAGGCTCT 354

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QY 100 uGlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLe 120
Db 355 TCAGCAAAATGGGCTCTCAGTCTCTCAGAGACAGACAGACGCTTGACACCAATCT 414
QY 120 uAsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnG 140
Db 415 AAATACATGAGCAGCACCATCTACAGTACTGGAAAAGTTTGTAAACCCAGATAATCCACA 474
QY 140 uCysLeuLeuGluGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnG 160
Db 475 ATGCTATTACTTGAACACAGGTTGATGAATTAATGGCAACAGTTTAGACTACATGA 534
QY 160 uArgLeuTyrAlaTyrPgluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTy 180
Db 535 GAGGCTCTGGGCTTGGAAAGCTGGAGATCTGAGGTCGGCAACGAGCTGAGGCCATTATA 594
QY 180 rGluGluTyrValValLeu-LysAsnGluMetAlaArgAlaAsnHisTyrGlu-AspTyr 199
Db 595 TGAAGAGTATGTGGTCTTGAATAATGAGATGCGCAAGAGCAATCATTTATGAGGGACTAT 654
QY 200 -GlyAspTyrTrpArgGlyAsp 206
Db 655 GGGGATATTGGAGAGGAGAC 676
RESULT 7
BG722079
LOCUS BG722079 Homo sapiens cDNA clone IMAGE:4830668 5',
DEFINITION mRNA sequence.
ACCESSION BG722079
VERSION BG722079.1 GI:14001266
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NIH-MGC http://mhc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10752 row: c column: 21
High quality sequence stop: 633.
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Location/Qualifiers
1..635
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4830668"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcagag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',
size-selected for average insert size 2-2 kb and
normalized to 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 202 a 131 c 144 g 158 t
ORIGIN
Alignment Scores:
Pred. No.: 5.85e-102 Length: 635

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BF789159
LOCUS BF789159 965 bp mRNA linear EST 12-JAN-2001
DEFINITION 62105037F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4223312
5', mRNA sequence.
ACCESSION BF789159
VERSION BF789159.1 GI:12094195
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 965)
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14W9811 row: i column: 09
High quality sequence stop: 676.
Location/Qualifiers
1..965
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4223312"
/lab_host="NCI_CGAP_Kid14"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. 1"
BASE COUNT 286 a 213 c 253 g 212 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 1..89e-88 Length: 965
Score: 864.00 Matches: 182
Percent Similarity: 80.49% Conservative: 16
Best local Similarity: 73.98% Mismatches: 45
Query Match: 20.14% Indels: 5
DB: 10 Gaps: 2

US-09-635-501-2 (1-805) x BF789159 (1-965)

QY 1 MetSerSerSerTrpLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
Db 21 ATGTCAGCTCCTCGCTGCTCTTCAGCCT- GTTGCTGTACTACTGCTCAGTCCGTC 79
QY 21 IleGluGluAlaAlaThrPheLeuAspLysPheAsnHisGluAlaGlnSerPhe 40
Db 80 ACCGAGGAATGCCAGACATTTTAAACACTTTAATCAGAGCTGAAGACCTGTCT 139
QY 41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
Db 140 TATCAAGTTCACTTCTTTCGATTAATACTAATCTAATCTAATCTAATCTAATCTA 199
QY 61 AsnMetAsnAsnAlaGlnAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80
Db 200 AAGATGAGTGGCTGCGACCAAAATGGTCTGCTTTTATGAAGACAGCTAAGACTGCC 259
QY 81 GlnMetTyrProGluGluIleGlnAsnLeuThrValLysLeuGluLeuGlnAlaLeu 100
Db 260 CAAAGTTTCTCTACAGAAATCCAGACTCCGATCATCAACGGTCACTACAGGCCCTT 319
QY 101 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120

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Db 320 CAGCAAGTGGGTCTTCACACTCTCAGCAGACAGCAACAAACAGTTGAACACAATCTG 379
QY 121 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140
Db 380 AACACCATGAGCACCATTACAGTACTGAAAGATTTGCACCAACCAAGACCAAGAA 439
QY 141 CysLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160
Db 440 TGTATTACTTTCAGCAGGATTTGATGAATAATGCGACAGACAGACTCAACTCT 499
QY 161 ArgLeuTyrAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180
Db 500 AGGCTCTGGCATGGAGGGCTGGAGGCTGGAGTGGCAAGCAGCTGAGGCGGTGTAT 559
QY 181 GluGluTyrValLeuLysAsnGluMetAla-ArgAlaAsnHisTyrGluAspTyrGln 200
Db 560 GAAGAGTATGTGCTCTGAAACAGAGATGGCAAGAGCAACAATATACCACTATGG 619
QY 200 YAspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArg 220
Db 620 GGATTATTGGAGGGGACTATGACGACAGAGGAGCAGATGG-TACAACATATAACCCGTA 678
QY 220 yGlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLe 240
Db 679 ACAGTGATTGAGA---TGTGAACGTACTTCGCAGAAA---TCAGCATGGGTGAGCCTCT 732
QY 240 uHisAlaTyrValArg 245
Db 733 TCATGCTATGTGAGG 748

RESULT 10
AA162058
LOCUS
DEFINITION
ms31hl1.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:608613 5' similar to SW:ACE_MOUSE P09470
ANGIOTENSIN-CONVERTING ENZYME PRECURSOR, SOMATIC ; mRNA sequence.
ACCESSION AA162058
VERSION AA162058.1 GI:1739055
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 555)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:374045
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 446.
Location/Qualifiers
1..555
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:608613"
/clone_lib="Stratagene mouse skin (#937313)"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
FEATURES
source

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RESULT 13				
BW030353				
LOCUS	BW030353	556 bp	mRNA	linear
DEFINITION	48973 MARC 2BOV BOS taurus cDNA 5'			EST 05-NOV-2001
ACCESSION	BW030353			

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VERSION  BM030353.1  GI:16743923
KEYWORDS
SOURCE   Bos taurus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
          Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 556)
AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
          Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
          G.L., Heaton,M.P., Laegreid,W., Rohrer,G.A., Chitko-McKown,C.G.,
          Pertea,G., Holt,I., Karameycheva,S., Liang,F., Quackenbush,J. and
          Keefe,J.W.
TITLE     Sequence evaluation of four pooled-tissue normalized bovine cdna
          libraries and construction of a gene index for cattle
JOURNAL   Genome Res. 11 (4), 626-630 (2001)
MEDLINE   21180013
COMMENT   Contact: Smith TPL
          USDA, ARS, US Meat Animal Research Center
          PO Box 166, Clay Center, NE 68933-0166, USA
          Tel: 402 762 4366
          Fax: 402 762 4390
          Email: smith@mail.marc.usda.gov
          Single pass sequencing. Bases called and alt_trimmed with phred
          v0.980904.e. Vector identified by cross_match with the -minscore 18
          and -minmatch 12 options.
          PCR Primers
          FORWARD: AGGAAACAGCTATGACCAT
          BACKWARD: GTTTCCTCAGTCAGCAG
          Plate: 120 row: B column: 16
          Seq primer: ATTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source           1..556
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 2B0V"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site 1: XbaI; Site 2: XhoI;
                     Library made from pooled tissue from testis, thymus,
                     semitendinosus muscle, longissimus muscle, pancreas,
                     adrenal, and endometrium."
BASE COUNT  178 a 111 c 145 g 122 t
ORIGIN
Alignment Scores:
Pred. No.:      1.3e-75      Length:      556
Score:          749.50      Matches:     142
Percent Similarity: 86.02%      Conservative: 18
Best Local Similarity: 76.34%      Mismatches: 25
Query Match:    17.47%      Indels:      1
DB:             10          Gaps:         1

US-09-635-501-2 (1-805) x BM030353 (1-556)
QY  71  AlaPheLeuLysGluGlnSerThrLeuAlaGlnMetTyrProLeuGlnGluLeuAsn 90
      ||||| :||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
      2  GCCTTTATGAGACAGTCCCGGATGGCCAAACTTACTCCTCAGTGAAGAAATTCAGAA 61
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY  91  LeuThrValLysLeuGlnLeuAlaLeuGlnGlnAsnGlySerSerValLeuSerGlu 110
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
      62  CTCACACTCAAGCGTCAATTTGAGAGCCCTTCAGCATAGCGGACCTCAGCGCTCTGGCA 121
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY  111 AspLysSerLysArgLeuAsnThrIleLeuAsnThrMetSerThrIleTyrSerThrGly 130
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
      122  GAGAAGAGCAACAGATTGAACACGATTCTAAATAAATGAGCACCACCTACAGTACTGG 181
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY  131 LysValCysAsnProAspAsnProGlnGluCysLeuLeuLeuGluProGlyLeuAsnGlu 150
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
      182  AAGATTGAGCCCA---AATACACAGGAGTGTCTAGCCTTGAACCGAGTTTATGATGAC 238
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY  151 IleMetAlaAsnSerLeuAspTyrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSer 170
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

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Db  239  ATAATGAAACACAGACAGACTACAAATCGGAGGCTCTGGGCTTGGGAAGGCTGGAGGGCT 298
QY  171  GluValGlyLysGlnLeuArgProLeuTyrGluGluTyrValValLeuLysAsnGluMet 190
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db  299  GAAATTTGGCAACCACTAAGGCCATTGTATGAAGAGTATGTGCTCTAGAAAATGAGATG 358
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY  191  AlaArgAlaAsnHisTyrGluAspTyrGlyAspTyrTrpArgGlyAspTyrGluValAsn 210
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
      359  GCAAGAGCCACAAATATGAGGACTACGGGACTATGGAGAGGGGATTATGAGTGACT 418
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY  211  GlyValAspGlyTyrAspTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPhe 230
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
      419  GGGCGAGGGGACTATGACTACAGCCCTGACCATGTGATGAAGATGTGGAACGACCTTT 478
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY  231  GluGluIleLysProLeuTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsn 250
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
      479  GCAGAGATTAAACCATATATGAACACTTCATGCTATGTGAGGCGCAAGATTGATGCAT 538
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY  251  AlaTyrProSerTyrIle 256
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
      539  ACCTACCCCTTCCTATATC 556
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
RESULT 14
BG772384
LOCUS   602722306F1 NIH_MGC-97 Homo sapiens cdna clone IMAGE:4839289 5',
        mRNA sequence.
ACCESSION  BG772384
VERSION    BG772384.1  GI:14083037
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 741)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-remail.nih.gov
           Tissue procurement: Miklos Palkovics, M.D., Ph.D.
           CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
           Toshituki and Piero Carninci (RIKEN)
           CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LNL at:
           http://image.llnl.gov
           Plate: LLM10774 row: k column: 02
           High quality sequence stop: 581.
FEATURES             Location/Qualifiers
     source           1..741
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4839289"
                     /clone_lib="NIH_MGC_97"
                     /lab_host="DH10B"
                     /note="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgaag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',
                     size selected for average insert size 2.2 kb and
                     normalized to 5x. This is a primary library enriched
                     for full-length clones and constructed using the
                     cap-trapper method (Carninci, in preparation). Library
                     constructed by M. Brownstein (NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT  212 a 188 c 165 g 176 t
ORIGIN
Alignment Scores:
Pred. No.:      3.03e-73      Length:      741
Score:          730.50      Matches:     169
Percent Similarity: 87.88%      Conservative: 5

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```
Best Local Similarity: 85.35% Mismatches: 11
Query Match: 17.02% Indels: 13
DB: 10 Gaps: 4

US-09-635-501-2 (1-805) x BG772384 (1-741)

QY 1 MetSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
Db 58 ATGTCAGCTCTTCCTGGCTCTTCCTCAGCCTTGTGCTAACTGCTCAGTCACCC 117
QY 21 ILeGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
Db 118 ATTGAGGAACAGCCAGACATTTTGGACAAGTTTAAACACCAAGGCGGAGCCTGTC 177
QY 41 TTTGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
Db 178 TATCAAGTTCACCTGCTCTTGGAAATATACACCAATTAATGAGGAGATGCCAA 237
QY 61 AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80
Db 238 AACATGAATAATGCTGGGACAAATGCTCTGCTTATACGGAACAGTCCACACTGCC 297
QY 81 Gln-MetTyrProLeuGlnGlnLeuGlnAsnLeuThrValLysLeuGlnLeuAlaLe 100
Db 298 CAATATGTATCCACTACAGAAATTCAGAAATCTCACAGTCAAGCTTCAGCTGCGGCTCT 357
QY 100 uGlnGlnAsn---GlySerSerValLeuSerGluAspLysSerLys-ArgLeuAsnThrI 119
Db 358 TCAGCACACACTGGCTCTTCAGTCTCTCAGAGACAGACAGCAACGGTTGACACAA 417
QY 119 leLeu-AsnThr-MetSerThrIleTyrSerThrGly-LysValCysAsnProAspAsnP 138
Db 418 TTCTCAATACACATGAGCACCACATCTACAGTACTGGAACAGCTCTGTAACCCAGATAATC 477
QY 138 roGlnGluCysLeuLeuGluProGlyLeuAsnGlu-IleMetAlaAsnSerLeuAsp 157
Db 478 CACAAAGTCTTATCTTGAACAGGTTTGATGACACTATGCACTATGCACTTTAGAC 537
QY 158 TyrAsn---GluArgLeuTrpAlaTrpGluSer-TrpArgSerGluValAlaGlyLysGlnLe 176
Db 538 TACCAACTGACGAGGCTCTGGGCTTGGGAAAGCCTGGAGATCT---GCAGGTGCTGCAGC 594
QY 176 uArg-----ProLeuTyrGlu-GluTyrValValLeu 186
Db 595 ACCGTGAGGCCACTTATATGAGGAGTATGTGGTCTT 632

RESULT 15
BI826471
LOCUS 603076177F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5167987 5',
DEFINITION mRNA sequence.
ACCESSION BI826471
VERSION BI826471.1 GI:15938021
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 800)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgebb@remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Prepared by: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1417 row: j column: 20
High quality sequence stop: 797.
```

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FEATURES
Source
1. .800
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/Note="Organ: brain; Vector: pCMV-SPORT6; Site: 1; NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC library."
BASE COUNT 169 a 244 c 230 g 157 t
ORIGIN
Alignment Scores: 3 04e-68 Length: 800
Pred. No.: 687.50 Matches: 128
Score: 68.30% Conservative: 53
Percent Similarity: 48.30% Mismatches: 81
Best Local Similarity: 16.02% Indels: 4
Query Match: 10 Gaps: 3
DB: 3
US-09-635-501-2 (1-805) x BI826471 (1-800)
QY 230 PheGluGluLysProLeuTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMet 249
Db 9 TTCAGGAGGTGCGACACCTACCTCAGCTGCTACGTGCGCGGCGCCTGCAC 68
QY 250 AsnAlaTyr--ProSerTyrIleSerProIleGlyCysLeuProAlaHisLeuGly 268
Db 69 CGTCACTACGGGGCCGACACATCACTGGAGGGGCCCATTCCTCTCCTACCTCTGGGG 128
QY 269 AspMetTrpGlyArgPheTrpTrpAsnLeuTyrSerLeuThrValProPheGlyGlnLys 288
Db 129 AACATGTGGCGCAGACCTGCTCCAACATCTATGACTGTGTGCTGCTCCCTCCCTTCAGCC 188
QY 289 ProAsnIleAspValThrAspAlaMetValAspGlnAlaTrpAspAlaGlnArgIlePhe 308
Db 189 CCCTCGATGGACACACAGAGGCTATGCTAAAGCAGGGCTGGAGCCCGCCAGGAGATGTTT 248
QY 309 LysGluAlaGluLysPhePheValSerValGlyLeuProAsnMetThrGlnGlyPheTrp 328
Db 249 AAGGAGGCTGATGATTTCTTCACTCCCTGGGGCTGCTGCCGTGCTCCTGAGTTCTGG 308
QY 329 GluAsnSerMetLeuThrAspProGlyAsnValGlnLysAlaValCysHisProThrAla 348
Db 309 AACAAAGTCGATGTGGAGAGAACCAACGACGGGGGAGGTGTCTGCCACGCTCGGCC 368
QY 349 TrpAspLeuGlyLysGly---AspPheArgIleLeuMetCysThrLysValThrMetAsp 367
Db 369 TGGGACTTCTACACGGCAAGGACTTCCGGATCAAGCAGTGCACCCCGTGAACCTGGAG 428
QY 368 AspPheLeuThrAlaHisHisGluMetGlyHisIleGlnTyrAspMetAlaTyrAlaAla 387
Db 429 GACCTGTGTGGGCCACACCAAGAAATGGGCACATCCAGTATTTTCATGCAGTACAAAGAC 488
QY 388 GlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPheHisGluAlaValGlyLeu 407
Db 489 TTACCTCTGGCCTTGGAGGAGGTGCCAACCCGCTTCATGAGGCATTTGGGAGCATG 548
QY 408 MetSerSerAlaAlaThrProLysHisLeuLysSerIleGlyLeuLeuSerProAsp 427
Db 549 CTAGCCCTCTCAGTGTCTAGCCCAAGCACCCTGCACAGTCTCAACCTCTCAGGAGTGGAG 608
QY 428 PheGlnGluAspAsnGluThrGluIleAsnPheLeuLysGlnAlaLeuThrIleVal 447
Db 609 GGTGGCGCGCAC---GAGCATGACATCAACTTTCTGTGATGAAGATGGCCCTTGACAAGATC 665
```

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QY 448 GlyThrLeuProPheThrTyrMetLeuGluLysTyrArgTyrMetValPheLysGlyGlu 467
Db 666 GCCTTTATCCCTTCAGCTACCTCGTCGATCAGTGGCGCTGGAGGTATTGAT-GGAAGC 724
QY 468 IleProLysAspGlnTrpMetLysLysTyrTrpGluMetLysArgGluIleValGlyVal 487
Db 725 ATCACCAGGAGAACTATAACCCAGGAGTGTGGAGCCTCAGGCTGAAAGTACCAGGGCCT 784
QY 488 ValGluProValPro 492
Db 785 CTGCCCCCAGTGCCC 799

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Search completed: October 9, 2002, 19:18:04
Job time : 1506 secs

